A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING, IMAGING AND TREATING VARIOUS CANCERS

FIELD OF THE INVENTION

This invention relates, in part, to newly developed assays for detecting, diagnosing, monitoring, staging, prognosticating, imaging and treating various cancers, particularly gynecologic cancer including ovarian, uterine endometrial and breast cancer, and lung cancer.

BACKGROUND OF THE INVENTION

The American Cancer Society has estimated that over 560,000 Americans will die this year from cancer. Cancer is the second leading cause of death in the United States, exceeded only by heart disease. It has been estimated that over one million new cancer cases will be diagnosed in 1999 alone.

In women, gynecologic cancers account for more than one-fourth of the malignancies.

Of the gynecologic cancers, breast cancer is the most common. According to the Women's Cancer Network, 1 out of every 8 women in the United States is as risk of developing breast cancer, and 1 out of every 28 women are at risk of dying from breast cancer. Approximately 77% of women diagnosed with breast cancer are over the age of 50. However, breast cancer is the leading cause of death in women between the ages of 40 and 55.

Carcinoma of the ovary is another very common gynecologic cancer. Approximately one in 70 women will develop ovarian cancer during her lifetime. An estimated 14,500 deaths in 1995 resulted from ovarian cancer. It causes more deaths than any other cancer of the female reproductive system. Ovarian cancer often does not cause any noticeable

symptoms. Some possible warning signals, however, are an enlarged abdomen due to an accumulation of fluid or vague digestive disturbances (discomfort, gas or distention) in women over 40; rarely there will be abnormal vaginal bleeding. Periodic, complete pelvic examinations are important; a Pap test does not detect ovarian cancer. Annual pelvic exams are recommended for women over 40.

Also common in women is endometrial cancer or carcinoma of the lining of the uterus. According to the Women's Cancer Center endometrial cancer accounts for approximately 13% of all malignancies in women. There are about 34,000 cases of endometrial cancer diagnosed in the United States each year.

Uterine sarcoma is another type of uterine malignancy much more rare as compared to other gynecologic cancers. In uterine sarcoma, malignant cells start growing in the muscles or other supporting tissues of the uterus. Sarcoma of the uterus is different from cancer of the endometrium, a disease in which cancer cells start growing in the lining of the uterus. This uterine cancer usually begins after menopause. Women who have received therapy with high-dose X-rays (external beam radiation therapy) to their pelvis are at a higher risk to develop sarcoma of the uterus. These X-rays are sometimes given to women to stop bleeding from the uterus.

Lung cancer is the second most prevalent type of cancer for both men and women in the United States and is the most common cause of cancer death in both sexes. Lung cancer can result from a primary tumor originating in the lung or a secondary tumor which has spread from another organ such as the bowel or breast. Primary lung cancer is divided into three main types; small cell lung cancer; non-small cell lung cancer; and mesothelioma. Small cell lung cancer is also called "Oat Cell" lung cancer because the cancer cells are a distinctive oat shape. There are three types of non-small cell lung cancer. These are grouped together because they behave in a similar way and respond to treatment differently to small

cell lung cancer. The three types are squamous cell carcinoma, adenocarcinoma, and large cell carcinoma. Squamous cell cancer is the most common type of lung cancer. It develops from the cells that line the airways. Adenocarcinoma also develops from the cells that line the airways. However, adenocarcinoma develops from a particular type of cell that produces mucus (phlegm). Large cell lung cancer has been thus named because the cells look large and rounded when they are viewed under a microscope. Mesothelioma is a rare type of cancer which affects the covering of the lung called the pleura. Mesothelioma is often caused by exposure to asbestos.

Procedures used for detecting, diagnosing, monitoring, staging, and prognosticating each of these types of cancer are of critical importance to the outcome of the patient. In all cases, patients diagnosed early in development of the cancer generally have a much greater five-year survival rate as compared to the survival rate for patients diagnosed with a cancer which has metastasized. New diagnostic methods which are more sensitive and specific for early detection of various types of cancer are clearly needed.

In the present invention methods are provided for detecting, diagnosing, monitoring, staging, prognosticating, *in vivo* imaging and treating selected cancers including, but not limited to, gynecologic cancers such as ovarian, breast endometrial and/or uterine cancer, and lung cancer via detection of a Cancer Specific Genes (CSGs). Nine CGSs have been identified and refer, among other things, to native proteins expressed by the genes comprising the polynucleotide sequences of any of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8 or 9. In the alternative, what is meant by the nine CSGs as used herein, means the native mRNAs encoded by the genes comprising any of the polynucleotide sequences of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8 or 9 or it can refer to the actual genes comprising any of the polynucleotide sequences of SEQ ID NO: 1, 2, 3, 4,

5, 6, 7, 8 or 9. Fragments of the CSGs such as those depicted in SEQ ID NO:10, 11, 12, 13 or 14 can also be detected.

Other objects, features, advantages and aspects of the present invention will become apparent to those of skill in the art from the following description. It should be understood, however, that the following description and the specific examples, while indicating preferred embodiments of the invention are given by way of illustration only. Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following description and from reading the other parts of the present disclosure.

SUMMARY OF THE INVENTION

Toward these ends, and others, it is an object of the present invention to provide a method for diagnosing the presence of selected cancers by analyzing for changes in levels of CSG in cells, tissues or bodily fluids compared with levels of CSG in preferably the same cells, tissues, or bodily fluid type of a normal human control, wherein a change in levels of CSG in the patient versus the normal human control is associated with the selected cancer. For the purposes of this invention, by "selected cancer" it is meant to include gynecologic cancers such as ovarian, breast, endometrial and uterine cancer, and lung cancer.

Further provided is a method of diagnosing metastatic cancer in a patient having a selected cancer which is not known to have metastasized by identifying a human patient suspected of having a selected cancer that has metastasized; analyzing a sample of cells, tissues, or bodily fluid from such patient for CSG; comparing the CSG levels in such cells, tissues, or bodily fluid with levels of CSG in preferably the same cells, tissues, or bodily fluid type of a normal human control, wherein an increase in CSG levels in the patient

versus the normal human control is associated with a cancer which has metastasized.

Also provided by the invention is a method of staging selected cancers in a human patient by identifying a human patient having such cancer; analyzing a sample of cells, tissues, or bodily fluid from such patient for CSG; comparing CSG levels in such cells, tissues, or bodily fluid with levels of CSG in preferably the same cells, tissues, or bodily fluid type of a normal human control sample, wherein an increase in CSG levels in the patient versus the normal human control is associated with a cancer which is progressing and a decrease in the levels of CSG is associated with a cancer which is regressing or in remission.

Further provided is a method of monitoring selected cancers in patients for the onset of metastasis. The method comprises identifying a human patient having a selected cancer that is not known to have metastasized; periodically analyzing a sample of cells, tissues, or bodily fluid from such patient for CSG; comparing the CSG levels in such cells, tissues, or bodily fluid with levels of CSG in preferably the same cells, tissues, or bodily fluid type of a normal human control sample, wherein an increase in CSG levels in the patient versus the normal human control is associated with a cancer which has metastasized.

Further provided is a method of monitoring the change in stage of selected cancers in humans having such cancer by looking at levels of CSG. The method comprises identifying a human patient having a selected cancer; periodically analyzing a sample of cells, tissues, or bodily fluid from such patient for CSG; comparing the CSG levels in such cells, tissue, or bodily fluid with levels of CSG in preferably the same cells, tissues, or bodily fluid type of a normal human control sample, wherein an increase in CSG levels in the patient versus the normal human control is associated with a cancer which is progressing and a decrease in the levels of

CSG is associated with a cancer which is regressing or in remission.

Further provided are antibodies against CSG or fragments of such antibodies which can be used to detect or image localization of CSG in a patient for the purpose of detecting or diagnosing selected cancers. Such antibodies can be polyclonal or monoclonal, or prepared by molecular biology techniques. The term "antibody", as used herein and throughout the instant specification is also meant to include aptamers and single-stranded oligonucleotides such as those derived from an *in vitro* evolution protocol referred to as SELEX and well known to those skilled in the art. Antibodies can be labeled with a variety of detectable labels including, but not limited to, radioisotopes and paramagnetic metals. These antibodies or fragments thereof can also be used as therapeutic agents in the treatment of diseases characterized by expression of a CSG. In therapeutic applications, the antibody can be used without or with derivatization to a cytotoxic agent such as a radioisotope, enzyme, toxin, drug or a prodrug.

Other objects, features, advantages and aspects of the present invention will become apparent to those of skill in the art from the following description. It should be understood, however, that the following description and the specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only. Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following description and from reading the other parts of the present disclosure.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to diagnostic assays and methods, both quantitative and qualitative for detecting, diagnosing, monitoring, staging and prognosticating selected

cancers by comparing levels of CSG with those of CSG in a normal human control. What is meant by levels of CSG as used herein is levels of the native protein expressed by the gene comprising the polynucleotide sequence of any of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8 or 9. In the alternative, what is meant by levels of CSG as used herein is levels of the native mRNA encoded by the gene comprising any of the polynucleotide sequence of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8 or 9 or levels of the gene comprising any of the polynucleotide sequences of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8 or 9. Fragments of CSGs such as those depicted in SEQ ID NO: 10, 11, 12, 13 and 14 can also be detected. Such levels are preferably measured in at least one of cells, tissues and/or bodily fluids, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for diagnosing over-expression of CSG protein compared to normal control bodily fluids, cells, or tissue samples may be used to diagnose the presence of selected cancers. What is meant by "selected cancers" as used herein is a gynecologic cancer such as ovarian, breast, endometrial or uterine cancer, or lung case.

Any of the 9 CSGs can be measured alone in the methods of the invention, or all together or any combination thereof. However, for methods relating to gynecologic cancers including ovarian, breast, endometrial and uterine cancer, it is preferred that levels of CSG comprising SEQ ID NO:1 or a fragment thereof be determined. Exemplary fragments of this CSG which can be detected are depicted in SEQ ID NO: 10, 11, 12, and 13. For methods relating to lung cancer and gynecologic cancers including ovarian, endometrial and uterine, it is preferred that levels of CSG comprising SEQ ID NO:2 or 9 be determined. Fragments of this CSG such as that depicted in SEQ ID NO:14 can also be detected. For methods relating to ovarian cancer, determination of levels of CSG comprising SEQ ID NO:3 is also preferred.

All the methods of the present invention may optionally include measuring the levels of other cancer markers as well as CSG. Other cancer markers, in addition to CSG, useful in the present invention will depend on the cancer being tested and are known to those of skill in the art.

Diagnostic Assays

The present invention provides methods for diagnosing the presence of selected cancers by analyzing for changes in levels of CSG in cells, tissues or bodily fluids compared with levels of CSG in cells, tissues or bodily fluids of preferably the same type from a normal human control, wherein a change in levels of CSG in the patient versus the normal human control is associated with the presence of a selected cancer.

Without limiting the instant invention, typically, for a quantitative diagnostic assay a positive result indicating the patient being tested has cancer is one in which cells, tissues or bodily fluid levels of the cancer marker, such as CSG, are at least two times higher, and most preferably are at least five times higher, than in preferably the same cells, tissues or bodily fluid of a normal human control.

The present invention also provides a method of diagnosing metastases of selected cancers in a patient having a selected cancer which has not yet metastasized for the onset of metastasis. In the method of the present invention, a human cancer patient suspected of having a selected cancer which may have metastasized (but which was not previously known to have metastasized) is identified. This is accomplished by a variety of means known to those of skill in the art. For example, in the case of ovarian cancer, patients are typically diagnosed with ovarian cancer following surgical staging and monitoring of CA125 levels. Traditional detection methods are also available and well known for other selected cancers which can be diagnosed by determination of CSG levels in a patient.

In the present invention, determining the presence of CSG levels in cells, tissues or bodily fluid, is particularly useful for discriminating between a selected cancer which has not metastasized and a selected cancer which has metastasized. Existing techniques have difficulty discriminating between cancers which have metastasized and cancers which have not metastasized and proper treatment selection is often dependent upon such knowledge.

In the present invention, the cancer marker levels measured in such cells, tissues or bodily fluid is CSG, and are compared with levels of CSG in preferably the same cells, tissue or bodily fluid type of a normal human control. That is, if the cancer marker being observed is CSG in serum, this level is preferably compared with the level of CSG in serum of a normal human patient. An increase in the CSG in the patient versus the normal human control is associated with a cancer which has metastasized.

Without limiting the instant invention, typically, for a quantitative diagnostic assay a positive result indicating the cancer in the patient being tested or monitored has metastasized is one in which cells, tissues or bodily fluid levels of the cancer marker, such as CSG, are at least two times higher, and most preferably are at least five times higher, than in preferably the same cells, tissues or bodily fluid of a normal patient.

Normal human control as used herein includes a human patient without cancer and/or non cancerous samples from the patient; in the methods for diagnosing or monitoring for metastasis, normal human control may also include samples from a human patient that is determined by reliable methods to have a selected cancer which has not metastasized.

Staging

The invention also provides a method of staging selected cancers in human patients. The method comprises identifying a human patient having a selected cancer and analyzing a

sample of cells, tissues or bodily fluid from such human patient for CSG. Then, the method compares CSG levels in such cells, tissues or bodily fluid with levels of CSG in preferably the same cells, tissues or bodily fluid type of a normal human control sample, wherein an increase in CSG levels in the human patient versus the normal human control is associated with a cancer which is progressing and a decrease in the levels of CSG is associated with a cancer which is regressing or in remission.

Monitoring

Further provided is a method of monitoring selected cancers in humans for the onset of metastasis. The method comprises identifying a human patient having a selected cancer that is not known to have metastasized; periodically analyzing a sample of cells, tissues or bodily fluid from such human patient for CSG; comparing the CSG levels in such cells, tissues or bodily fluid with levels of CSG in preferably the same cells, tissues or bodily fluid type of a normal human control sample, wherein an increase in CSG levels in the human patient versus the normal human control is associated with a cancer which has metastasized.

Further provided by this invention is a method of monitoring the change in stage of selected cancers in humans having such cancers. The method comprises identifying a human patient having a selected cancer; periodically analyzing a sample of cells, tissues or bodily fluid from such human patient for CSG; comparing the CSG levels in such cells, tissues or bodily fluid with levels of CSG in preferably the same cells, tissues or bodily fluid type of a normal human control sample, wherein an increase in CSG levels in the human patient versus the normal human control is associated with a cancer which is progressing in stage and a decrease in the levels of CSG is associated with a cancer which is regressing in stage or in remission.

Monitoring such patient for onset of metastasis is periodic and preferably done on a quarterly basis. However, this may be more or less frequent depending on the cancer, the particular patient, and the stage of the cancer.

Assay Techniques

Assay techniques that can be used to determine levels of gene expression, such as CSG of the present invention, in a sample derived from a patient are well known to those of skill in the art. Such assay methods include radioimmunoassays, reverse transcriptase PCR (RT-PCR) assays, immunohistochemistry assays, *in situ* hybridization assays, competitive-binding assays, Western Blot analyses, ELISA assays and proteomic approaches. Among these, ELISAs are frequently preferred to diagnose a gene's expressed protein in biological fluids.

An ELISA assay initially comprises preparing an antibody, if not readily available from a commercial source, specific to CSG, preferably a monoclonal antibody. In addition a reporter antibody generally is prepared which binds specifically to CSG. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, for example horseradish peroxidase enzyme or alkaline phosphatase.

To carry out the ELISA, antibody specific to CSG is incubated on a solid support, e.g. a polystyrene dish, that binds the antibody. Any free protein binding sites on the dish are then covered by incubating with a non-specific protein such as bovine serum albumin. Next, the sample to be analyzed is incubated in the dish, during which time CSG binds to the specific antibody attached to the polystyrene dish. Unbound sample is washed out with buffer. A reporter antibody specifically directed to CSG and linked to horseradish peroxidase is placed in the dish resulting in binding of the reporter antibody to any monoclonal antibody bound to CSG. Unattached reporter antibody is then washed out. Reagents for

peroxidase activity, including a colorimetric substrate are then added to the dish. Immobilized peroxidase, linked to CSG antibodies, produces a colored reaction product. The amount of color developed in a given time period is proportional to the amount of CSG protein present in the sample. Quantitative results typically are obtained by reference to a standard curve.

A competition assay may be employed wherein antibodies specific to CSG attached to a solid support and labeled CSG and a sample derived from the host are passed over the solid support and the amount of label detected attached to the solid support can be correlated to a quantity of CSG in the sample.

Nucleic acid methods may be used to detect CSG mRNA as a marker for selected cancers. Polymerase chain reaction (PCR) and other nucleic acid methods, such as ligase chain reaction (LCR) and nucleic acid sequence based amplification (NASABA), can be used to detect malignant cells for diagnosis and monitoring of the various selected malignancies. For example, reverse-transcriptase PCR (RT-PCR) is a powerful technique which can be used to detect the presence of a specific mRNA population in a complex mixture of thousands of other mRNA species. In RT-PCR, an mRNA species is first reverse transcribed to complementary DNA (cDNA) with use of the enzyme reverse transcriptase; the cDNA is then amplified as in a standard PCR reaction. RT-PCR can thus reveal by amplification the presence of a single species of mRNA. Accordingly, if the mRNA is highly specific for the cell that produces it, RT-PCR can be used to identify the presence of a specific type of cell.

Hybridization to clones or oligonucleotides arrayed on a solid support (i.e. gridding) can be used to both detect the expression of and quantitate the level of expression of that gene. In this approach, a cDNA encoding the CSG gene is fixed to a substrate. The substrate may be of any suitable type including but not limited to glass, nitrocellulose, nylon

or plastic. At least a portion of the DNA encoding the CSG gene is attached to the substrate and then incubated with the analyte, which may be RNA or a complementary DNA (cDNA) copy of the RNA, isolated from the tissue of interest. Hybridization between the substrate bound DNA and the analyte can be detected and quantitated by several means including but not limited to radioactive labeling or fluorescence labeling of the analyte or a secondary molecule designed to detect the hybrid. Quantitation of the level of gene expression can be done by comparison of the intensity of the signal from the analyte compared with that determined from known standards. The standards can be obtained by *in vitro* transcription of the target gene, quantitating the yield, and then using that material to generate a standard curve.

Of the proteomic approaches, 2D electrophoresis is a technique well known to those in the art. Isolation of individual proteins from a sample such as serum is accomplished using sequential separation of proteins by different characteristics usually on polyacrylamide gels. First, proteins are separated by size using an electric current. The current acts uniformly on all proteins, so smaller proteins move farther on the gel than larger proteins. The second dimension applies a current perpendicular to the first and separates proteins not on the basis of size but on the specific electric charge carried by each protein. Since no two proteins with different sequences are identical on the basis of both size and charge, the result of a 2D separation is a square gel in which each protein occupies a unique spot. Analysis of the spots with chemical or antibody probes, or subsequent protein microsequencing can reveal the relative abundance of a given protein and the identity of the proteins in the sample.

The above tests can be carried out on samples derived from a variety of patients' cells, bodily fluids and/or tissue extracts (homogenates or solubilized tissue) such as from

tissue biopsy and autopsy material. Bodily fluids useful in the present invention include blood, urine, saliva or any other bodily secretion or derivative thereof. Blood can include whole blood, plasma, serum or any derivative of blood.

***In Vivo* Antibody Use**

Antibodies against CSG can also be used *in vivo* in patients suspected of suffering from a selected cancer including lung cancer or gynecologic cancers such as ovarian, breast, endometrial or uterine cancer. Specifically, antibodies against a CSG can be injected into a patient suspected of having a selected cancer for diagnostic and/or therapeutic purposes. The use of antibodies for *in vivo* diagnosis is well known in the art. For example, antibody-chelators labeled with Indium-111 have been described for use in the radioimmunoscintographic imaging of carcinoembryonic antigen expressing tumors (Sumerdon et al. Nucl. Med. Biol. 1990 17:247-254). In particular, these antibody-chelators have been used in detecting tumors in patients suspected of having recurrent colorectal cancer (Griffin et al. J. Clin. Onc. 1991 9:631-640). Antibodies with paramagnetic ions as labels for use in magnetic resonance imaging have also been described (Lauffer, R.B. Magnetic Resonance in Medicine 1991 22:339-342). Antibodies directed against CSGs can be used in a similar manner. Labeled antibodies against a CSG can be injected into patients suspected of having a selected cancer for the purpose of diagnosing or staging of the disease status of the patient. The label used will be selected in accordance with the imaging modality to be used. For example, radioactive labels such as Indium-111, Technetium-99m or Iodine-131 can be used for planar scans or single photon emission computed tomography (SPECT). Positron emitting labels such as Fluorine-19 can be used in positron emission tomography. Paramagnetic ions such as Gadlinium (III) or Manganese (II) can used in magnetic resonance imaging (MRI). Localization of the label permits determination of the spread

of the cancer. The amount of label within an organ or tissue also allows determination of the presence or absence of cancer in that organ or tissue.

For patients diagnosed with a selected cancer, injection of an antibody against a CSG can also have a therapeutic benefit. The antibody may exert its therapeutic effect alone. Alternatively, the antibody is conjugated to a cytotoxic agent such as a drug, toxin or radionuclide to enhance its therapeutic effect. Drug monoclonal antibodies have been described in the art for example by Garnett and Baldwin, *Cancer Research* 1986 46:2407-2412. The use of toxins conjugated to monoclonal antibodies for the therapy of various cancers has also been described by Pastan et al. *Cell* 1986 47:641-648. Yttrium-90 labeled monoclonal antibodies have been described for maximization of dose delivered to the tumor while limiting toxicity to normal tissues (Goodwin and Meares Cancer Supplement 1997 80:2675-2680). Other cytotoxic radionuclides including, but not limited to Copper-67, Iodine-131 and Rhenium-186 can also be used for labeling of antibodies against CSGs.

Antibodies which can be used in these *in vivo* methods include both polyclonal and monoclonal antibodies and antibodies prepared via molecular biology techniques. Antibody fragments and aptamers and single-stranded oligonucleotides such as those derived from an *in vitro* evolution protocol referred to as SELEX and well known to those skilled in the art can also be used.

The present invention is further described by the following examples. These examples are provided solely to illustrate the invention by reference to specific embodiments. The exemplifications, while illustrating certain aspects of the invention, do not portray the limitations or circumscribe the scope of the disclosed invention.

EXAMPLES

Example 1:

Identification of CSGs were carried out by a systematic analysis of data in the LIFESEQ database available from Incyte Pharmaceuticals, Palo Alto, CA, using the data mining Cancer Leads Automatic Search Package (CLASP) developed by diaDexus LLC, Santa Clara, CA.

The CLASP performs the following steps: selection of highly expressed organ specific genes based on the abundance level of the corresponding EST in the targeted organ versus all the other organs; analysis of the expression level of each highly expressed organ specific genes in normal, tumor tissue, disease tissue and tissue libraries associated with tumor or disease. Selection of the candidates demonstrating component ESTs were exclusively or more frequently found in tumor libraries. The CLASP allows the identification of highly expressed organ and cancer specific genes. A final manual in depth evaluation is then performed to finalize the CSGs selection.

Table 1: CSG Sequences

SEQ ID NO:	Clone ID	Gene ID
1	16656542	234617
2	1283171	332459
3	1649377	481154
4	236044H1	none assigned
5	none assigned	255687
6	none assigned	251313
7	none assigned	12029
8	none assigned	251804

The following examples are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail.

Routine molecular biology techniques of the following example can be carried out as described in standard laboratory manuals, such as Sambrook et al., MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989).

Example 2: Relative Quantitation of Gene Expression

Real-Time quantitative PCR with fluorescent Taqman probes is a quantitation detection system utilizing the 5'-3' nuclease activity of Taq DNA polymerase. The method uses an internal fluorescent oligonucleotide probe (Taqman) labeled with a 5' reporter dye and a downstream, 3' quencher dye. During PCR, the 5'-3' nuclease activity of Taq DNA polymerase releases the reporter, whose fluorescence can then be detected by the laser detector of the Model 7700 Sequence Detection System (PE Applied Biosystems, Foster City, CA, USA).

Amplification of an endogenous control is used to standardize the amount of sample RNA added to the reaction and normalize for Reverse Transcriptase (RT) efficiency. Either cyclophilin, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) or 18S ribosomal RNA (rRNA) is used as this endogenous control. To calculate relative quantitation between all the samples studied, the target RNA levels for one sample were used as the basis for comparative results (calibrator). Quantitation relative to the "calibrator" can be obtained using the standard curve method or the comparative method (User Bulletin #2: ABI PRISM 7700 Sequence Detection System).

The tissue distribution and the level of the target gene for every example in normal and cancer tissue were evaluated. Total RNA was extracted from normal tissues, cancer tissues, and from cancers and the corresponding matched adjacent tissues. Subsequently, first strand cDNA was prepared with reverse transcriptase and the polymerase chain reaction was done using primers and Taqman probe specific to each target gene. The results are analyzed using the ABI PRISM 7700

Sequence Detector. The absolute numbers are relative levels of expression of the target gene in a particular tissue compared to the calibrator tissue.

Measurement of Ovr110; Clone ID16656542; Gene ID 234617 (SEQ ID NO:1, 10, 11, 12 or 13)

The absolute numbers depicted in Table 2 are relative levels of expression of Ovr110 (SEQ ID NO:1 or a fragment thereof as depicted in SEQ ID NO:10, 11, 12, or 13) in 12 normal different tissues. All the values are compared to normal stomach (calibrator). These RNA samples are commercially available pools, originated by pooling samples of a particular tissue from different individuals.

Table 2: Relative Levels of Ovr110 Expression in Pooled Samples

Tissue	NORMAL
colon	0.00
endometrium	8.82
kidney	7.19
liver	0.36
ovary	1.19
pancreas	21.41
prostate	2.79
small intestine	0.03
spleen	0.00
0000000000000stoma	1.00
testis	8.72
uterus	0.93

The relative levels of expression in Table 2 show that Ovr110 is expressed at comparable levels in most of the normal tissues analyzed. Pancreas, with a relative expression level of 21.41, endometrium (8.82), testis (8.72), and kidney (7.19) are the only tissues expressing high levels of Ovr110 mRNA.

The absolute numbers in Table 2 were obtained analyzing pools of samples of a particular tissue from different individuals. They can not be compared to the absolute numbers originated from RNA obtained from tissue samples of a single individual in Table 3.

The absolute numbers depicted in Table 3 are relative levels of expression of Ovr110 in 73 pairs of matching samples. All the values are compared to normal stomach (calibrator). A matching pair is formed by mRNA from the cancer sample for a particular tissue and mRNA from the normal adjacent sample for that same tissue from the same individual. In addition, 15 unmatched cancer samples (from ovary and mammary gland) and 14 unmatched normal samples (from ovary and mammary gland) were also tested.

Table 3: Relative Levels of Ovr110 Expression in Individual Samples

Sample ID	Tissue	Cancer	Matching Normal Adjacent	Normal
Ovr103X	Ovary 1	86.22	0.53	
Ovr1040O	Ovary 2	168.31		
Ovr1157	Ovary 3	528.22		
Ovr63A	Ovary 4	1.71		
Ovr773O	Ovary 5	464.65		
Ovr1005O	Ovary 6	18.32		
Ovr1028	Ovary 7	7.78		
Ovr1118	Ovary 8	0.00		
Ovr130X	Ovary 9	149.09		
Ovr638A	Ovary 10	3.14		
OvrA1B	Ovary 11	21.26		
OvrA1C	Ovary 12	1.83		
OvrC360	Ovary 13	0.52		
Ovr18GA	Ovary 14			1.07
Ovr20GA	Ovary 15			1.88
Ovr25GA	Ovary 16			2.52
Ovr206I	Ovary 17			2.51
Ovr32RA	Ovary 18			3.01

Ovr35GA	Ovary 19			5.17
Ovr40G	Ovary 20			0.45
Ovr50GB	Ovary 21			2.69
OvrC087	Ovary 22			0.47
OvrC179	Ovary 23			1.46
OvrC004	Ovary 24			4.99
OvrC007	Ovary 25			13.36
OvrC109	Ovary 26			6.61
MamS516	Mammary Gland 1	16.39	13.74	
MamS621	Mammary Gland 2	826.70	4.60	
MamS854	Mammary Gland 3	34.60	18.30	
Mam59X	Mammary Gland 4	721.57	27.00	
MamS079	Mammary Gland 5	80.73	5.10	
MamS967	Mammary Gland 6	6746.90	72.80	
MamS127	Mammary Gland 7	7.00	20.00	
MamB011X	Mammary Gland 8	1042.00	29.00	
Mam12B	Mammary Gland 9	1342.00		
Mam82XI	Mammary Gland 10	507.00		
MamS123	Mammary Gland 11	24.85	4.24	
MamS699	Mammary Gland 12	84.74	5.54	
MamS997	Mammary Gland 13	482.71	11.84	
Mam162X	Mammary Gland 14	15.73	10.59	

MamA06X	Mammary Gland 15	1418.35	8.20	
Mam603X	Mammary Gland 16	294.00		
Mam699F	Mammary Gland 17	567.40	86.60	
Mam12X	Mammary Gland 18	425.00	31.00	
MamA04	Mammary Gland 19			2.00
Mam42DN	Mammary Gland 20	46.05	31.02	
Utr23XU	Uterus 1	600.49	27.95	
Utr85XU	Uterus 2	73.52	18.83	
Utr135XO	Uterus 3	178.00	274.00	
Utr141XO	Uterus 4	289.00	26.00	
CvxNKS54	Cervix 1	2.47	0.61	
CvxKS83	Cervix 2	1.00	2.00	
CvxNKS18	Cervix 3	1.00	0.00	
CvxNK23	Cervix 4	5.84	14.47	
CvxNK24	Cervix 5	20.32	33.13	
End68X	Endometrium 1	167.73	544.96	
End8963	Endometrium 2	340.14	20.89	
End8XA	Endometrium 3	1.68	224.41	
End65RA	Endometrium 4	303.00	5.00	
End8911	Endometrium 5	1038.00	74.00	
End3AX	Endometrium 6	6.59	1.69	
End4XA	Endometrium 7	0.43	15.45	

End5XA	Endometrium 8	17.81	388.02	
End10479	Endometrium 9	1251.60	31.10	
End12XA	Endometrium 10	312.80	33.80	
Kid107XD	Kidney 1	2.68	29.65	
Kid109XD	Kidney 2	81.01	228.33	
Kid10XD	Kidney 3	0.00	15.30	
Kid6XD	Kidney 4	18.32	9.06	
Kid11XD	Kidney 5	1.38	20.75	
Kid5XD	Kidney 6	30.27	0.19	
Liv15XA	Liver 1	0.00	0.45	
Liv42X	Liver 2	0.81	0.40	
Liv94XA	Liver 3	12.00	2.16	
Lng LC71	Lung 1	5.45	3.31	
LngAC39	Lung 2	1.11	0.00	
LngBR94	Lung 3	4.50	0.00	
LngSQ45	Lung 4	15.03	0.76	
LngC20X	Lung 5	0.00	1.65	
LngSQ56	Lung 6	91.77	8.03	
ClnAS89	Colon 1	0.79	7.65	
ClnC9XR	Colon 2	0.03	0.00	
ClnRC67	Colon 3	0.00	0.00	
ClnSG36	Colon 4	0.81	0.35	
ClnTX89	Colon 5	0.00	0.00	
ClnSG45	Colon 6	0.00	0.06	
ClnTX01	Colon 7	0.00	0.00	
Pan77X	Pancreas 1	0.89	2.62	
Pan71XL	Pancreas 2	3.99	0.12	
Pan82XP	Pancreas 3	59.92	28.44	
Pan92X	Pancreas 4	17.21	0.00	

StoAC93	Stomach 1	7.54	6.43	
StoAC99	Stomach 2	19.49	3.19	
StoAC44	Stomach 3	3.62	0.37	
SmI21XA	Small Intestine 1	0.00	0.00	
SmIH89	Small Intestine 2	0.00	0.00	
Bld32XK	Bladder 1	0.00	0.21	
Bld46XK	Bladder 2	0.36	0.32	
BldTR17	Bladder 3	0.28	0.00	
Tst39X	Testis	11.24	2.24	
Pro84XB	Prostate 1	2.60	24.30	
Pro90XB	Prostate 2	1.40	2.00	

0.00= Negative

Table 2 and Table 3 represent a combined total of 187 samples in 16 different tissue types. In the analysis of matching samples, the higher levels of expression were in mammary gland, uterus, endometrium and ovary, showing a high degree of tissue specificity for the gynecologic tissues. Of all the samples different than those mentioned before analyzed, only a few samples (Kid109XD, LngSQ56, and Pan82XP) showed high levels of expression of Ovr110.

Furthermore, the level of mRNA expression was compared in cancer samples and the isogenic normal adjacent tissue from the same individual. This comparison provides an indication of specificity for the cancer stage (e.g. higher levels of mRNA expression in the cancer sample compared to the normal adjacent). Table 3 shows overexpression of Ovr110 in 15 of 16 mammary gland cancer tissues compared with their respective normal adjacent (mammary gland samples MamS516, MamS621, MamS854, Mam59X, MamS079, MamS967, MamB011X, MamS123, MamS699, MamS997, Mam162X, MamA06X, Mam699F, Mam12X, and Mam42DN).

There was overexpression in the cancer tissue for 94% of the mammary gland matching samples tested.

For uterus, Ovr110 is overexpressed in 3 of 4 matching samples (uterus samples Utr23XU, Utr85XU, and Utr141XO). There was overexpression in the cancer tissue for 75% of the uterus matching samples analyzed.

For endometrium, Ovr110 is overexpressed in 6 of 10 matching samples (endometrium samples End8963, End65RA, End8911, End3AX, End10479, and End12XA). There was overexpression in the cancer tissue for 60% of the endometrium matching samples.

For ovary, Ovr110 shows overexpression in 1 of 1 matching sample. For the unmatched ovarian samples, 8 of 12 cancer samples show expression values of Ovr110 higher than the median (2.52) for the normal unmatched ovarian samples. There was overexpression in the cancer tissue for 67% of the unmatched ovarian samples.

Altogether, the level of tissue specificity, plus the mRNA overexpression in most of the matching samples tested are indicative of Ovr110 (including SEQ ID NO:1, 10, 11, 12 or 13) being a diagnostic marker for gynecologic cancers, specifically, mammary gland or breast, uterine, ovarian and endometrial cancer.

Measurement of Ovr114; Clone ID1649377; Gene ID 481154 (SEQ ID NO:3)

The numbers depicted in Table 4 are relative levels of expression in 12 normal tissues of Ovr114 compared to pancreas (calibrator). These RNA samples were obtained commercially and were generated by pooling samples from a particular tissue from different individuals.

Table 4: Relative Levels of Ovr114 Expression in Pooled Samples

Tissue	Normal
Colon	2.3
Endometrium	7.6
Kidney	0.5
Liver	0.6
Ovary	5.2
Pancreas	1.0
Prostate	2.1
Small Intestine	1.3
Spleen	2.4
Stomach	1.5
Testis	15.8
Uterus	8.8

The relative levels of expression in Table 4 show that Ovr114 mRNA expression is detected in all the pools of normal tissues analyzed.

The tissues shown in Table 4 are pooled samples from different individuals. The tissues shown in Table 5 were obtained from individuals and are not pooled. Hence the values for mRNA expression levels shown in Table 4 cannot be directly compared to the values shown in Table 5.

The numbers depicted in Table 5 are relative levels of expression of Ovr114 compared to pancreas (calibrator), in 46 pairs of matching samples and 27 unmatched tissue samples. Each matching pair contains the cancer sample for a particular tissue and the normal adjacent tissue sample for that same tissue from the same individual. In cancers (for example, ovary) where it was not possible to obtain normal adjacent samples from the same individual, samples from a different normal individual were analyzed.

Table 5: Relative Levels of Ovr114 Expression in Individual Samples

Tissue	Sample ID	Cancer Type	Cancer	Borderline Malignant	Normal & Matching Normal Adjacent
Ovary 1	Ovr1037O/1038O	Papillary serous adenocarcinoma, G3	17.04		3.93
Ovary 2	OvrG021SPI/SN2	Papillary serous adenocarcinoma	1.62		4.34
Ovary 3	OvrG010SP/SN	Papillary serous adenocarcinoma	0.50		1.12
Ovary 4	OvrA081F/A082D	Mucinous tumor, low malignant potential		0.84	0.96
Ovary 5	OvrA084/A086	Mucinous tumor, grade G-B, borderline		5.24	6.00
Ovary 6	Ovr14604A1C	Serous cystadenofibroma, low malignancy		5.33	
Ovary 7	Ovr14638A1C	Follicular cysts, low malignant potential		8.11	
Ovary 8	Ovr1040O	Papillary serous adenocarcinoma, G2	13.27		
Ovary 9	Ovr1157O	Papillary serous adenocarcinoma	106.08		
Ovary 10	Ovr1005O	Papillary serous endometricarcinoma	77.04		
Ovary 11	Ovr1028O	Ovarian carcinoma	14.78		
Ovary 12	Ovr14603A1D	Adenocarcinoma	22.23		

Ovary 13	Ovr9410C360	Endometrioid adenocarcinoma	4.74		
Ovary 14	Ovr1305X	Papillary serous adenocarcinoma	96.49		
Ovary 15	Ovr773O	Papillary serous adenocarcinoma	8.40		
Ovary 16	Ovr988Z	Papillary serous adenocarcinoma	6.40		
Ovary 17	Ovr9702C018GA	Normal Cystic			12.06
Ovary 18	Ovr2061	Normal left atrophic, small cystic			10.11
Ovary 19	Ovr9702C020GA	Normal-multiple ovarian cysts			12.70
Ovary 20	Ovr9702C025GA	Normal-hemorrhage CL cysts			22.09
Ovary 21	Ovr9701C050GB	Normal-multiple ovarian cysts			9.01
Ovary 22	Ovr9701C087RA	Normal-small follicle cysts			1.86
Ovary 23	Ovr9702C032RA				7.81
Ovary 24	Ovr9701C109RA	Normal			1.50
Ovary 25	Ovr9411C057R	Benign large endometriotic cyst			5.22
Ovary 26	Ovr9701C179a	Normal			3.09
Ovary 27	Ovr1461O	Serous cystadenofibroma, no malignancy			3.53
Ovary 28	Ovr9701C035GA	Normal			6.32

Ovary 29	Ovr9702C007RA	Normal			0
Ovary 30	Ovr9701C087RA	Normal-small follicle cysts			1.97
Ovary 31	Ovr9411C109	Normal			9.49
Ovary 32	Ovr9701C177a	Normal-cystic follicles			3.85
Endometrium 1	End14863A1A/A2A	Moderately differ. Endome. carcinoma/NAT	1.30		0.70
Endometrium 2	End9709C056A/55A	Endometrial adenocarcinoma/NAT	1.83		11.90
Endometrium 3	End9704C281A/2A	Endometrial adenocarcinoma/NAT	13.32		7.76
Endometrium 4	End9705A125A/6A	Endometrial adenocarcinoma/NAT	3.62		3.34
Mammary Gland 1	Mam00042D01/N01		3.13		0.76
Mammary Gland 2	MamS99-522A/B		4.45		0.45
Mammary Gland 3	Mam1620F/1621F		0.74		1.91
Mammary Gland 4	Mam4003259a/g		3.48		2.00
Uterus 1	Utr850U/851U	Stage 1 endometrial cancer/NAT	46.96		11.96
Uterus 2	Utr233U96/234U96	Adenocarcinoma/NAT	20.02		5.90
Uterus 3	Utr1359O/1358O	Tumor/NAT	10.23		7.74
Uterus 4	Utr1417O/1418O	Malignant tumor/NAT	7.52		4.92

Cervix 1	CvxVNM00083/83	Keratinizing squamous cell carcinoma	5.47		14.31
Cervix 2	CvxIND00023D/N	Large cell nonkeratinizing carcinoma	4.99		3.99
Cervix 3	CvxIND00024D/N	Large cell nonkeratinizing carcinoma	10.14		14.22
Bladder 1	Bld665T/664T		1.43		4.03
Bladder 2	Bld327K/328K	Papillary transitional cell carcinoma/NAT	1.15		0.99
Kidney 1	Kid4003710C/F		0.03		0.35
Kidney 2	Kid1242D/1243D		1.61		0.14
Lung 1	Lng750C/751C	Metastatic osteogenic sarcoma/NAT	2.44		5.73
Lung 2	Lng8890A/8890B	Cancer/NAT	1.11		5.19
Lung 3	Lng9502C109R/10R		1.99		0.80
Liver 1	Liv1747/1743	Hepatocellular carcinoma/NAT	0.67		1.07
Liver 2	LivVNM00175/175	Cancer/NAT	15.46		2.85
Skin 1	Skn2S9821248A/B	Secondary malignant melanoma	2.83		0.70
Skin 2	Skn4005287A1/B2		0.91		4.02
Small Int. 1	SmI9802H008/009		0.87		0.82
Stomach 1	Sto4004864A4/B4	Adenocarcinoma/NAT	0.81		1.22
Stomach 2	StoS9822539A/B	Adenocarcinoma/NAT	1.22		1.39

Stomach 3	StoS99728A/C	Malignant gastrointestinal stromal tumor	0.47		0.35
Prostate 1	Pro1012B/1013B	Adenocarcinoma/NAT	2.39		2.61
Prostate 2	Pro1094B/1095B		0.10		0.38
Pancreas 1	Pan776p/777p	Tumor/NAT	2.39		0.52
Pancreas 2	Pan824p/825p	Cystic adenoma	1.66		1.22
Testis 1	Tst239X/240X	Tumor/NAT	1.24		1.72
Colon 1	Cln9706c068ra/69ra	Adenocarcinoma/NAT	0.38		0.65
Colon 2	Cln4004732A7/B6	Adenocarcinoma/NAT	0.44		1.26
Colon 3	Cln4004695A9/B8		1.94		1.53
Colon 4	Cln9612B006/005	Asc. Colon, Cecum, adenocarcinoma	3.38		1.10
Colon 5	Cln9704C024R/25R	Adenocarcinoma/NAT	1.66		2.77

Table 4 and Table 5 represent a combined total of 129 samples in 17 human tissue types. Among 117 samples in Table 5 representing 16 different tissues high levels of expression are seen only in ovarian cancer samples. The median expression of Ovr114 is 14.03 (range: 0.5 - 106.08) in ovarian cancer and 4.34 (range: 0 - 22.09) in normal ovaries. In other words, the median expression levels of Ovr114 in cancer samples is increased 3.5 fold as compared with that of the normal ovarian samples. Five of 12 ovarian cancers (42%) showed increased expression relative to normal ovary (with 95% specificity). The median expression of Ovr114 in other gynecologic cancers is 4.99, and 2 out of 15 samples showed expression levels comparable with that in ovarian cancer. The median of the expression levels of Ovr114 in the rest of the cancer samples is 1.24, which is more than 11 fold less than that detected in ovarian cancer samples. No individual showed an expression level comparable to that of ovarian cancer samples (except Liver 2; LivVNM00175/175).

The 3.5 fold increase in expression in 42% of the individual ovarian cancer samples and no compatible expression in other non-gynecologic cancers is indicative of Ovr114 being a diagnostic marker for detection of ovarian cancer cells. It is believed that the Ovr114 marker may also be useful in detection of additional gynecologic cancers.

Measurement of Ovr115; Clone ID1283171; Gene ID 332459 (SEQ ID NO:2 or 14)

The numbers depicted in Table 6 are relative levels of expression Ovr115 compared to their respective calibrators. The numbers are relative levels of expression in 12 normal tissues of ovaries compared to Testis (calibrator). These RNA samples were obtained commercially and were generated by pooling samples from a particular tissue from different individuals.

Table 6: Relative Levels of Ovr115 Expression in Pooled Samples

Tissue	Normal
Colon	858.10
Endometrium	12.34
Kidney	3.76
Liver	0.00
Ovary	0.43
Pancreas	0.00
Prostate	8.91
Small Intestine	62.25
Spleen	0.00
Stomach	37.53
Testis	1.00
Uterus	47.67

The relative levels of expression in Table 6 show that Ovr115 mRNA expression is detected in all the 12 normal tissue pools analyzed.

The tissues shown in Table 6 are pooled samples from different individuals. The tissues shown in Table 7 were obtained from individuals and are not pooled. Hence the values for mRNA expression levels shown in Table 6 cannot be directly compared to the values shown in Table 7.

The numbers depicted in Table 7 are relative levels of expression of Ovr115 compared to testis (calibrator), in 46 pairs of matching samples and 27 unmatched tissue samples. Each matching pair contains the cancer sample for a particular tissue and the normal adjacent tissue sample for that same tissue from the same individual. In cancers (for example, ovary) where it was not possible to obtain normal adjacent samples from the same individual, samples from a different normal individual were analyzed.

Table 7: Relative Levels of Ovr115 Expression in Individual Samples

Tissue	Sample ID	Cancer Type	Cancer	Borderline Malignant	Normal & Matching Normal Adjacent
Ovary 1	Ovr1037O/1038O	Papillary serous adenocarcinoma, G3	193.34		0.24
Ovary 3	OvrG021SPI/SN2	Papillary serous adenocarcinoma	0.38		0.31
Ovary 4	OvrG010SP/SN	Papillary serous adenocarcinoma	231.25		0.45
Ovary 2	OvrA084/A086	Mucinous tumor, grade G-B, borderline		143.34	16.65
Ovary 5	OvrA081F/A082D	Mucinous tumor, low malignant potential		314.13	0
Ovary 19	Ovr14604A1C	Serous cystadenofibroma, low malignancy		299.87	
Ovary 26	Ovr14638A1C	Follicular cysts, low malignant potential		1278.32	
Ovary 6	Ovr1040O	Papillary serous adenocarcinoma, G2	144.25		
Ovary 22	Ovr9410C360	Endometrioid adenocarcinoma	0.29		
Ovary 23	Ovr1305X	Papillary serous adenocarcinoma	157.41		
Ovary 27	Ovr773O	Papillary serous adenocarcinoma	340.04		
Ovary 28	Ovr988Z	Papillary serous adenocarcinoma	464.75		

Ovary 7	Ovr1157O	Papillary serous adenocarcinoma	432.07		
Ovary 8	Ovr1005O	Papillary serous endometricarcinoma	74.23		
Ovary 9	Ovr1028O	Ovarian carcinoma	1408.79		
Ovary 10	Ovr14603A1D	Adenocarcinoma	0.00		
Ovary 11	Ovr9702C018GA	Normal Cystic			0.16
Ovary 12	Ovr2061	Normal left atrophic, small cystic			0.00
Ovary 13	Ovr9702C020GA	Normal-multiple ovarian cysts			0.00
Ovary 14	Ovr9702C025GA	Normal-hemorrhage CL cysts			0.00
Ovary 15	Ovr9701C050GB	Normal-multiple ovarian cysts			0.91
Ovary 16	Ovr9701C087RA	Normal-small follicle cysts			0.00
Ovary 17	Ovr9702C032RA				0.28
Ovary 18	Ovr9701C109RA	Normal			0.00
Ovary 20	Ovr9411C057R	Benign large endometriotic cyst			38.87
Ovary 21	Ovr9701C179a	Normal			0.08
Ovary 24	Ovr1461O	Serous cystadenofibroma, no malignancy			0.00
Ovary 25	Ovr9701C035GA	Normal			0.00
Ovary 29	Ovr9702C007RA	Normal			0.00

Ovary 30	Ovr9701C087RA	Normal-small follicle cysts			0.00
Ovary 31	Ovr9411C109	Normal			0.00
Ovary 32	Ovr9701C177a	Normal-cystic follicles			0.00
Uterus 1	Utr850U/851U	Stage 1 endometrial cancer/NAT	39.95		13.60
Uterus 2	Utr233U96/234U96	Adenocarcinoma/NAT	140.37		22.67
Uterus 3	Utr1359O/1358)	Tumor/NAT	16.45		32.50
Uterus 4	Utr1417O/1418O	Malignant tumor/NAT	288.52		5.29
Endometrium 1	End14863A1A/A2A	Moderately differ. Endome. carcinoma/NAT	2.61		6.24
Endometrium 2	End9709C056A/55A	Endometrial adenocarcinoma/NAT	2.10		49.40
Endometrium 3	End9704C281A/2A	Endometrial adenocarcinoma/NAT	480.77		19.22
Endometrium 4	End9705A125A/6A	Endometrial adenocarcinoma/NAT	322.07		31.08
Lung 1	Lng750C/751Ċ	Metastatic osteogenic sarcoma/NAT	38.81		7.36
Lung 2	Lng8890A/8890B	Cancer/NAT	690.12		14.71
Lung 3	Lng9502C109R/10R		1756.90		2.86
Skin 1	Skn2S9821248A/B	Secondary malignant melanoma	10.56		0.00
Skin 2	Skn4005287A1/B2		331.30		47.23
Prostate 1	Pro1012B/1013B	Adenocarcinoma/NAT	14.64		4.39

Prostate 2	Pro1094B/1095B		0.09		2.54
Bladder 1	Bld665T/664T		404.56		90.20
Bladder 2	Bld327K/328K	Papillary transitional cell carcinoma/NAT	77.35		177.37
Kidney 1	Kid4003710C/F		0.17		12.72
Kidney 2	Kid1242D/1243D		0.00		13.74
Mammary Gland 1	Mam1620F/1621F		0.27		0.12
Mammary Gland 2	Mam4003259a/g		5.71		0.00
Liver 1	Liv1747/1743	Hepatocellular carcinoma/NAT	0.14		0.69
Liver 2	LivVNM00175/175	Cancer/NAT	0.00		0.00
Small Int. 1	SmI9802H008/009		128.44		151.38
Stomach 1	Sto4004864A4/B4	Adenocarcinoma/NAT	303.01		116.72
Stomach 2	StoS9822539A/B	Adenocarcinoma/NAT	24.12		17.76
Stomach 3	StoS99728A/C	Malignant gastrointestinal stromal tumor	0.00		9.10
Pancreas 1	Pan776p/777p	Tumor/NAT	0.00		0.43
Pancreas 2	Pan824p/825p	Cystic adenoma	0.00		3.17
Testis 1	Tst239X/240X	Tumor/NAT	24.05		1.37
Colon 1	Cln9706c068ra/69ra	Adenocarcinoma/NAT	605.60		169.77
Colon 2	Cln4004732A7/B6	Adenocarcinoma/NAT	367.20		281.32

Colon 3	Cln4004695A9/B8		316.15		295.77
Colon 4	Cln9612B006/005	Asc. Colon. Cecum, adenocarcinoma	820.89		543.52
Colon 5	Cln9704C024R/25R	Adenocarcinoma/NAT	161.18		150.07
Cervix 1	CvxVNM00083/83	Keratinizing squamous cell carcinoma	738.17		1195.88
Cervix 2	CvxIND00023D/N	Large cell nonkeratinizing carcinoma	1473.04		1229.80
Cervix 3	CvxIND00024D/N	Large cell nonkeratinizing carcinoma	2877.48		1275.02

Table 6 and Table 7 represent a combined total of 129 samples in 17 human tissue types. Comparisons of the level of mRNA expression in ovarian cancer samples and the normal adjacent tissue from the same individuals or normal tissues from other individuals are shown in Table 7. Ovr115 was expressed at higher levels in 9 of 12 cancer tissues (75%), relative to the maximum level detected in all 21 normal or normal adjacent ovarian samples. All 4 of 4 (100%) ovarian tumors with borderline malignancy had elevated Ovr115 expression. The median expression in ovarian cancers (including the ones with borderline malignancy) was 212.30 while the median expression in normal ovaries was 0. When compared with their own normal adjacent tissue samples, expression levels of Ovr115 were also elevated in 3 of 3 (100%) lung cancers, 3 of 4 (75%) uterus cancers and 2 of 4 (50%) endometrial cancers.

The relatively high expression levels of Ovr115 in ovarian and other selected cancer samples is indicative of Ovr115 being a diagnostic marker for detection of ovarian, lung, uterine and endometrial cancer.

A homolog of Ovr115 has also been identified in public data base; g2597613 as gi|2507612|gb|U75329.1|HSU75329 Human serine protease mRNA, complete CDS. This homolog is depicted herein as SEQ ID NO:9. It is believed that SEQ ID NO:9 or the protein encoded thereby (SEQ ID NO:15) may also be useful as a diagnostic marker for detection of ovarian, lung, uterine and endometrial cancer in human patients.